

## FIGURE 1

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R35464 GGCCGGGTCG TTTCTCGCCT GGCTGGGATC GCTGCTCCTC TCTGGGGTCC 50
ORF    P G R F S P G W D R C S S L G S 16

R35464 TGGCCGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTGAA 100
ORF    W P A D R E R S I H D F C L V S K 33

R35464 GGTGGTGGGC AGATTCCGGG CCTCCATGCC TAGGTGGTGG TACAATGTCA 150
ORF    V V G R E R A S M P R W W Y N V T 50

R35464 CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAACAGC 200
ORF    D G S C Q L F V Y G G C D G N S 66

R35464 AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC 250
ORF    N N Y L T K E E C L K K C A T V T 83

R35464 AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT 300
ORF    E N A T G D L A T S R N A A D S S 100

R35464 CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTTCAGCGA 350
ORF    V P S A P R R Q D S * R P L Q R 116

R35464 TATGTTTCAA NTATTGNAAG AATAATTGCA CCGNCAACGN ATT----- 393
ORF    Y V S * I * R I I A P * T * 130

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## KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO: 12)

ORF = EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)

## FIGURE 2

R74593 GCAATAATTA CCTGACCAAG GAGGAGTGCC TCAAGAAATG TGCCACTGTC 50  
ORF Q \* L P D Q G G V P Q E M C H C H 17

R74593 ACAGAGAATG CCACGGGTGA CCTGGCCACC AGCAGGAATG CAGCGGATTC 100  
ORF R E C H G \* P G H Q Q E C S G F 33

R74593 CTCTGTCCCA AGTCTCCCAG AAGGCAGGAT TCTGAAGACC ACTCCAGCGA 150  
ORF L C P K S P R R Q D S E D H S S D 50

R74593 TATGTTCAAC TATGAAGAAT ACTGCACCGC CAACGCAGTC ACTGGGCCTT 200  
ORF M F N Y E E Y C T A N A V T G P C 67

R74593 GCCGTGCATC CTTCCCACGC TGGTACTTTG ACGTGGAGAG GAACTCCTGC 250  
ORF R A S F P R W Y F D V E R N S C 83

R74593 AATAACTTCA TCTATGGAGG CTGCCGGGGC AATAAGAACA GCTACCGCTC 300  
ORF N N F I Y G G C R G N K N S Y R S 100

R74593 TGAGGAGGCC TGCATGCTCC GCTGCTTCCG JCAGCAGGAG AATCCTCCCC 350  
ORF E E A C M L R C F R Q Q E N P P L 117

R74593 TGCCCCTTGG CTCAAAGGTG GTGGTTCTGG CCGGGGCTGT TTCGTGATGG 400  
ORF P L G S K V V V L A G A V S \* W 133

R74593 TGTTGATCCT TTTCTGGGG AGCNTCCATG GTCTTACTGA TTCCGGGTGG 450  
ORF C \* S F S W G A S M V L L I P G G 150

R74593 CAAGGAGGAA CCAGGAGCGT GCCCTGCGGA NCGTCTGGAG CTTCGGAGAT 500  
ORF K E E P G A C P A X R L E L R R \* 167

R74593 GACAAGGGNT 510  
ORF Q G 169

## KEY

R74593 = Nucleic acid sequence of EST R74593 (SEQ ID NO: 14)

ORF = EST R74593 Open Reading Frame Translation (SEQ ID NO: 15)

## FIGURE 3

R35464	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50												
N39798			TGGGANTC	GCTGCTCCTC	TCTGGGGTCC	28												
H94519	GCNGCG-CGT	TNNTCGCNT-	GCTGGGA-TC	GCTGCACCTC	TCTGGGGTCC	47												
R74593 corr.	-----	-----	-----	-----	-----	-----												
Consensus	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50												
Translation	A	G	S	F	L	A	W	L	G	S	L	L	L	S	G	V	-3	
R35464	TGGCCGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	100												
N39798	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	77												
H94519	NGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	96												
R74593 corr.	-----	-----	-----	-----	-----	-----												
Consensus	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	99												
Translation	L	A	A	D	R	E	R	S	I	H	D	E	C	L	Y	S	K	15
R35464	GGTGGTGGGC	AGATTCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	150												
N39798	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	127												
H94519	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	146												
R74593 corr.	-----	-----	-----	-----	-----	-----												
Consensus	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	149												
Translation	Y	Y	G	R	C	R	A	S	M	P	R	W	W	X	N	Y	T	32
R35464	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	200												
N39798	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	177												
H94519	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	196												
R74593 corr.	-----	-----	-----	-----	-----GC	2												
Consensus	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	199												
Translation	D	G	S	C	Q	L	E	Y	Y	G	G	C	D	G	N	S	48	
R35464	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTGAC	250												
N39798	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTGAC	227												
H94519	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTGAC	246												
R74593 corr.	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTGAC	52												
Consensus	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTGAC	249												
Translation	N	N	Y	L	T	K	E	E	C	L	K	K	C	A	T	V	T	65
R35464	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCT	300												
N39798	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCT	277												
H94519	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCT	296												
R74593 corr.	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCT	102												
Consensus	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCT	299												
Translation	E	N	A	T	G	D	L	A	T	S	R	N	A	A	D	S	S	82
R35464	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CTTGAAGACC	ACTTCAGCGA	350												
N39798	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTTCAGCGA	326												
H94519	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTTCAGCGA	345												
R74593 corr.	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTTCAGCGA	151												
Consensus	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTTCAGCGA	348												
Translation	V	P	S	A	P	R	R	Q	D	S	E	D	H	S	S	D	98	
R35464	TATGTTTCAA	NTATTGNAAG	AATAATTGCA	CCGNCACGN	ATT-----	393												
N39798	TATGTTTCAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	372												
H94519	TATGTTTCAA	CTA-TG-AAG	AATACTGGCA	CCGCCAACGC	AGTCACTGGG	392												
R74593 corr.	TATGTTTCAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	197												
Consensus	TATGTTTCAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	394												
Translation	M	F	N	Y	E	E	Y	C	T	A	N	A	V	T	G	113		

## FIGURE 3 (CONT)

R35464	-----	-----	-----	-----	-----	
N39798	CCTTGC-GTG	GAATCCTTTC	CCACGCTGGN	AATTNGACG	TTGAGAAGGA	421
H94519	CCT-GC-GTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GNCG	-----	427
R74593 corr.	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	243
Consensus	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	440
Translation	P C R A	S F	P R W Y	F D V	E R N	129
R35464	-----	-----	-----	-----	-----	
N39798	AC-----	-----	-----	-----	-----	423
H94519	-----	-----	-----	-----	-----	
R74593 corr.	ACTCCTGCAA	TAAC TTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	293
Consensus	ACTCCTGCAA	TAAC TTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	490
Translation	S C N	N F I	Y G G C	R G N	K N S	145
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	343
Consensus	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	540
Translation	Y R S E	E A C	M L R	C F R Q	Q E N	162
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCCTCCCTG	CCCCTGGCT	CAAAGGTGGT	GGTCTGGCC	GGGGCTGTTT	393
Consensus	TCCTCCCTG	CCCCTGGCT	CAAAGGTGGT	GGTCTGGCC	GGGGCTGTTT	590
Translation	P P L	P L G S	K V V	V L A	G A V S	179
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	443
Consensus	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	640
Translation	* W C	* S F	S W G A	S M V	L L I	195
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	GTCTGGAGCT	493
Consensus	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	GTCTGGAGCT	690
Translation	P G G K	E E P	G A C	P A * R	L E L	212
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCGGAGATGA	CAAGGGNT				511
Consensus	TCGGAGATGA	CAAGGGNT				708
Translation	R R *	Q G				217

## KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO.: 12)  
 N39798 = Nucleic acid sequence of EST N39798 (SEQ ID NO.: 17)  
 H94519 = Nucleic acid sequence of EST H94519 (SEQ ID NO.: 16)  
 R74593 corr. = Corrected version of (SEQ ID NO.: 14) G at b.p. 114  
 Consensus = Nucleic acid sequence for human bikunin (SEQ ID NO.: 9)  
 Translation = Amino acid Translation of Consensus (SEQ ID NO.: 10)

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Figure 4 A.

Schematic depicting the overlap of ESTs bearing homology to the cDNA sequence encoding placental bikunin

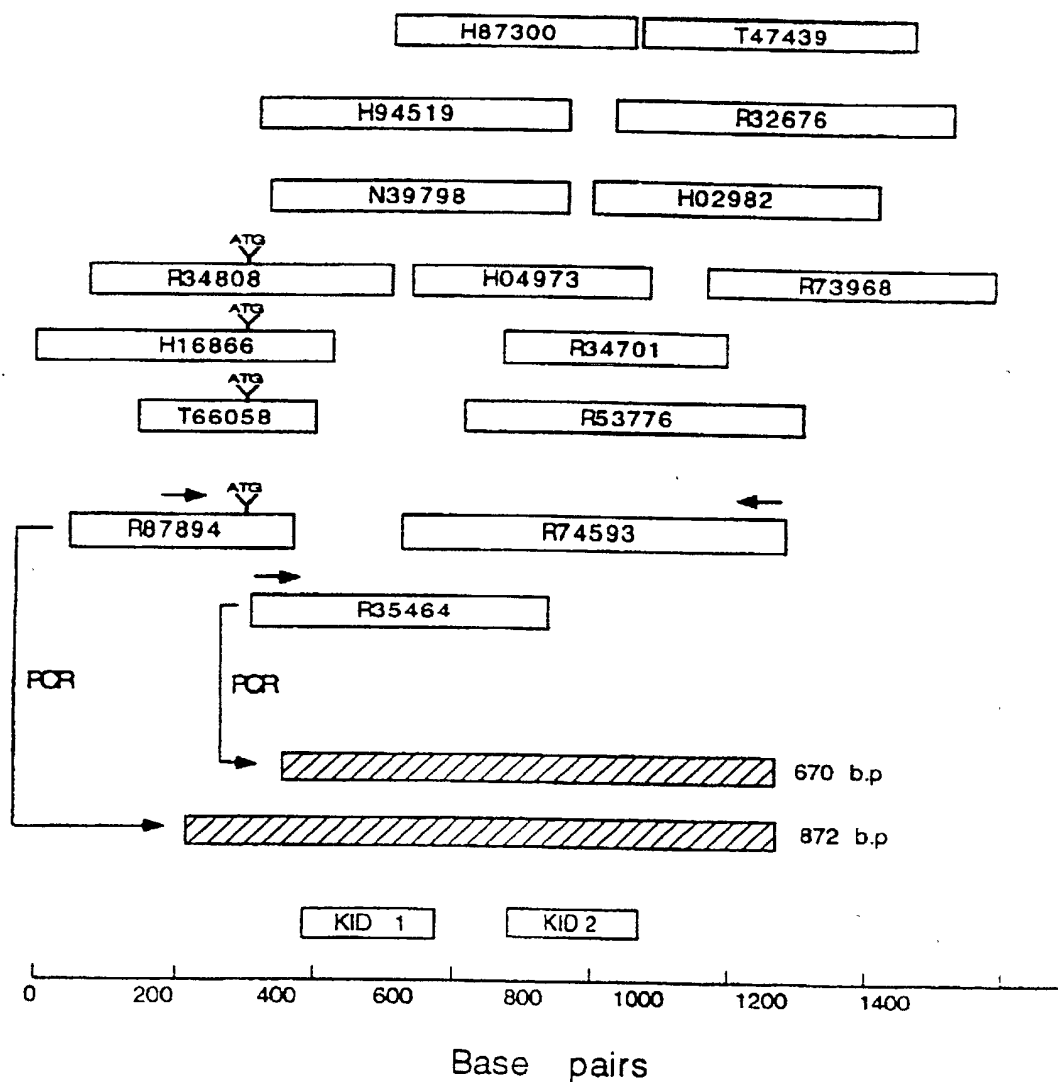
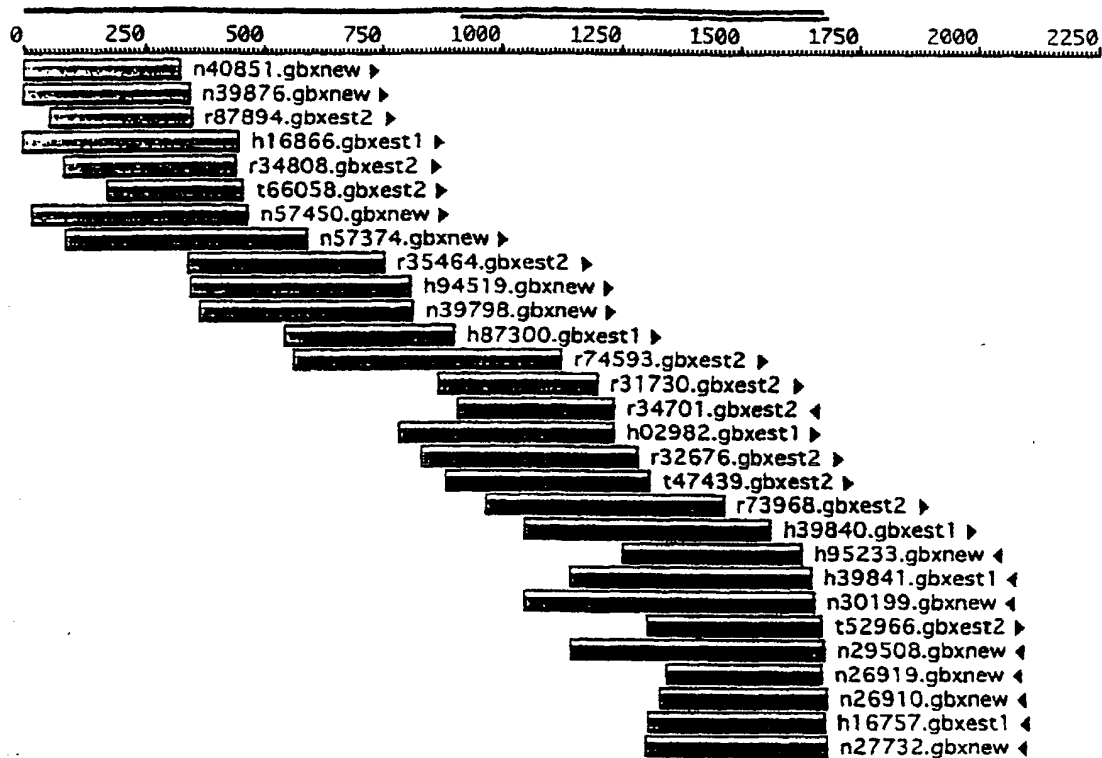


Figure 4B



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Figure 4C

	1				50
Bikunin	.....GCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
N40851	.....GCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
N39876	.....GCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
R87894	.....	.....	.....	.....	.....
H16866	.....GGCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCG.CT	CTGAACGGGN
R34808	.....	.....	.....	.....	.....
T66058	.....	.....	.....	.....	.....
N57450	.....	.....	.....T	TAGCGCGGCT	CTGAACGCNA
N57374	.....	.....	.....	.....	.....
R35464	.....	.....	.....	.....	.....
H94519	.....	.....	.....	.....	.....
N39798	.....	.....	.....	.....	.....
H87300	.....	.....	.....	.....	.....
R74593	.....	.....	.....	.....	.....
R31730	.....	.....	.....	.....	.....
R34701	.....	.....	.....	.....	.....
H02982	.....	.....	.....	.....	.....
R32676	.....	.....	.....	.....	.....
T47439	.....	.....	.....	.....	.....
R73968	.....	.....	.....	.....	.....
H39840	.....	.....	.....	.....	.....
H95233	.....	.....	.....	.....	.....
H39841	.....	.....	.....	.....	.....
N30199	.....	.....	.....	.....	.....
T52966	.....	.....	.....	.....	.....
N29508	.....	.....	.....	.....	.....
N26919	.....	.....	.....	.....	.....
N26910	.....	.....	.....	.....	.....
H16757	.....	.....	.....	.....	.....
N27732	.....	.....	.....	.....	.....

Figure 4C (Con't)

	51	100
Bikunin	GNA GGGCCG TTGAGTGTCT CAGGCGGCCA GGGCGCGAGT GAGGAGCAGA	
N40851	NGAGNCGCCG TTGAGTGTCT CAGGCGGCCA GGGCGCGAGT GAGGAGCAGA	
N39876	GCA.GGGCCG TTGAGTGTCT CAGGCGGCCA GGGCGCGAGT GAGGAGCAGA	
R87894	..... TTGAGTGTCT NAGGCGGCCA GGGCGCGAGT GAGGAGCAGA	
H16866	..ANGGGCCG TTGAGTGTCT CAGGCGGCC.A GGGCN.GAGT GAGGAGCAGA	
R34808	..... G GAGGAGCAGA	
T66058	.....	
N57450	GAAGNCGCCG TTGAGTGTCT CAGGCGGCCA GGGCGCGAGT GAGGAGCAGA	
N57374	..... AGA	
R35464	.....	
H94519	.....	
N39798	.....	
H87300	.....	
R74593	.....	
R31730	.....	
R34701	.....	
H02982	.....	
R32676	.....	
T47439	.....	
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	



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Figure 4C (Con't)

	101	150
Bikunin	CCCAGGCATC GCGCGCCGAG AAGNC GGGC GTCCCCACAC TGAAGGTCCG	
N40851	CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG	
N39876	CCCAGGCATC GCGCGCCGAG AAGNC.GGGC NTCCCCACAC TGAAGGTCCG	
R87894	CCCAGGCATC GCGCGCCGAG AAGGCCGGGC GTCCCCACAC TGAAGGTCCG	
H16866	CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG	
R34808	CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG	
T66058	.....	.....
N57450	CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG	
N57374	CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG	
R35464	.....	.....
H94519	.....	.....
N39798	.....	.....
H87300	.....	.....
R74593	.....	.....
R31730	.....	.....
R34701	.....	.....
H02982	.....	.....
R12676	.....	.....
T47439	.....	.....
R73968	.....	.....
H39840	.....	.....
H95233	.....	.....
H39841	.....	.....
N30199	.....	.....
T52966	.....	.....
N29508	.....	.....
N26919	.....	.....
N26910	.....	.....
H16757	.....	.....
N27732	.....	.....

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Figure 4C (Con't)

	151	200
Bikunin	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
N40851	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
N39876	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
R87894	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
H16866	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
R34808	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
T66058	..... ..	...GGACCCT CCCGGAGCGT
N57450	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
N57374	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT CCCGGAGCGT	
R35464	..... ..	
H94519	..... ..	
N39798	..... ..	
H87300	..... ..	
R74593	..... ..	
R31730	..... ..	
R34701	..... ..	
H02982	..... ..	
R32676	..... ..	
T47439	..... ..	
R73968	..... ..	
H39840	..... ..	
H95233	..... ..	
H39841	..... ..	
N30199	..... ..	
T52966	..... ..	
N29508	..... ..	
N26919	..... ..	
N26910	..... ..	
H16757	..... ..	
N27732	..... ..	

Figure 4C (Con't)

	201			250
Bikunin	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG .AGGGGCTTC
N40851	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG .AGGGGCTTC
N39876	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG .AGGGGCTTC
R87894	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG .AGGGGCTTC
H16866	.GGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG .AGGGGCTTC
R34808	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG GAGGGGCTTC
T66058	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	.GTCCGTTTG NAGGGGCTTC
N57450	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG .AGGGGCTTC
N57374	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTCCGTTTG .AGGGGCTTC
R35464	.....	.....	.....	.....
H94519	.....	.....	.....	.....
N39798	.....	.....	.....	.....
H87300	.....	.....	.....	.....
R74593	.....	.....	.....	.....
R31730	.....	.....	.....	.....
R34701	.....	.....	.....	.....
H02982	.....	.....	.....	.....
R32676	.....	.....	.....	.....
T47439	.....	.....	.....	.....
R73968	.....	.....	.....	.....
H39840	.....	.....	.....	.....
H95233	.....	.....	.....	.....
H39841	.....	.....	.....	.....
N30199	.....	.....	.....	.....
T52966	.....	.....	.....	.....
N29508	.....	.....	.....	.....
N26919	.....	.....	.....	.....
N26910	.....	.....	.....	.....
H16757	.....	.....	.....	.....
N27732	.....	.....	.....	.....

Figure 4C (Con't)

	251	300
Bikunin	CCGCACCT G ATCGCGAGAC CCCAACGGCT GGTGG CGTC GC TG CGCG	
N40851	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CGCG	
N39876	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CGCG	
R87894	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTNG.CGTC GC.TN.CGCG	
H16866	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTNG.CGTC GC.TGGCGCG	
R34808	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGGCGCT GC.TG.CGCG	
T66058	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GC.TG.CGCG	
N57450	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CGCG	
N57374	CCGGAACCTG ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GC.TG.CGCG	
R35464	.....	
H94519	.....	
N39798	.....	
H87300	.....	
R74593	.....	
R31730	.....	
R34701	.....	
H02982	.....	
R32676	.....	
T47439	.....	
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	

## Figure 4C (Con't)

	301		350
Bikunin	TC TCGGCTG AGCT GGCCA TGGCGCANT GTTGC GGGC T GAGGC GG		
N40851	TC.TCGGCTG AGCT.GGNCA TGTCG		
N39876	TC.TCGGCTG AGCT.GGCCA TGGCGCACT. G.TGCGGNGC T.GAGGC.G		
R87894	TC.TCGGCTG AGCTTGCCCA TGGCGCANT. GTTNC.GGGC T.NAGGC.GG		
H16866	TTCTCGGCTG AGCT.GGCCA TGGCGCANT. GTTGC.GNGC T.GAGGC.GG		
R34808	TCTTCGGCTG AGCTGGGCCA TGGCGCANTT GTTGC.GGGC T.GAGGC.GG		
T66058	TC.TCGGCTG AGCT.GGCCA TGGCGCANT. GTTGC.GNGC T.GAGGC.GG		
N57450	TC.TCGGCTG AGCT.GGCCA TGGCGCANT. GGTGC.GGGC TTGAGGC.GG		
N57374	TCCTCGGCTG AGCT.GGCCA TGGCGCANT. GGTGCCGNGC T.GAGGCCGG		
R35464	.....	.....	....GGCCGG
H94519	.....	.....	.....
N39798	.....	.....	.....
H87300	.....	.....	.....
R74593	.....	.....	.....
R31730	.....	.....	.....
R34701	.....	.....	.....
H02982	.....	.....	.....
R32676	.....	.....	.....
T47439	.....	.....	.....
R73968	.....	.....	.....
H39840	.....	.....	.....
H95233	.....	.....	.....
H39841	.....	.....	.....
N30199	.....	.....	.....
T52966	.....	.....	.....
N29508	.....	.....	.....
N26919	.....	.....	.....
N26910	.....	.....	.....
H16757	.....	.....	.....
N27732	.....	.....	.....

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Figure 4C (Con't)

	351	400
Bikunin	AC GG CG	TTTCTCG CC TGCTGGG A TCGCT GC T CCTCTCT
R87894	ACG.	
H16866	AC..CGNCGT	TTTCTCTCG. CCTTGCTGGG ATTGCTTGC TTCTNTCTG
R34808	ACGCGGNCG.	.TTTTTTCGN CCTTGCTGGG ATTCG.TTG. TTNCTCTCTN
T66058	...CGNCG.	.TTTCTCG. CC.TGCTGGG A.TCGCT.GC T.CCTCTCT.
N57450	ANN.NGCCG.	.TTTCTCG. CC.TGCTGGG A.TCGCT.GC T.CCTCTCT.
N57374	AG..GGCCGG	.TTTCTCG. CCTTGCTGGG A.TCGCT.GC T.CCTCTCTG
R35464	.....GTCTG.	.TTTCTCG. CCTGGCTGGG A.TCGCT.GC T.CCTCTCT.
H94519	.GCNCGCGG.	.TTNNTCG. CN.TGCTGGG A.TCGCT.GC A.CCTCTCT.
N39798	.....	.....CTGGG ANTCTGCT.GC T.CCTCTCT.
H87300	.....	.....
R74593	.....	.....
R31730	.....	.....
R34701	.....	.....
H02982	.....	.....
R32676	.....	.....
T47439	.....	.....
R73968	.....	.....
H39840	.....	.....
H95233	.....	.....
H39841	.....	.....
N30199	.....	.....
T52966	.....	.....
N29508	.....	.....
N26919	.....	.....
N26910	.....	.....
H16757	.....	.....
N27732	.....	.....

Figure 4C (Con't)

	401	450
Bikunin	GGGG TCCTG G CGGCCGA CCGA GAACG CA GCA TCC ACGACTT CT	
H16866	GGGGTTCCTG GG.CGGGCCGA CCGA.GAACG CA.GCA.TCC AAGAATTTT	
R34808	GGGGTTC.TG GGGNGGCCGA NCGA.GAACG CAAGCA.TTC ACGA.TTT	
T66058	GGGG.TCCTG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGANTT.CT	
N57450	GGGG.TCCTG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
N57374	GGGG.TCCTG G..CGGCCGA NCGAAGAANG CA.GCAATCC ANGAATTNCT	
R35464	GGGG.TCCTG G.CCGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
R94519	GGGG.TCGNG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
N39798	GGGG.TCCTG G..CGGCCGA CCGA.GAACG CA.GCA.TCC ACGACTT.CT	
H87300	.....	.....
R74593	.....	.....
R31730	.....	.....
R34701	.....	.....
H02982	.....	.....
R32676	.....	.....
T47439	.....	.....
R73968	.....	.....
H39840	.....	.....
H95233	.....	.....
H39841	.....	.....
N30199	.....	.....
T52966	.....	.....
N29508	.....	.....
N26919	.....	.....
N26910	.....	.....
H16757	.....	.....
N27732	.....	.....

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## Figure 4C (Con't)

	451	500
Bikunin	GCCTGGTGT CGAAGGT GG TGGGCAGATG CCGGG CCTC CATGCCTA G	
H16866	GCC	
T66058	TCCTGGTSTT CGAAGG	
N57450	GCCTGGTGT. CGAAGGT.GG TGGGCAG	
N57374	GCCTGGTGT CGAAAGTTGG TGGGCANATT CCGGGCCTT CATGNCTAAG	
R35464	GCCTGGTGT. CGAAGGT.GG TGGGCAGATT CCGGG.CCTC CATGCCTA.G	
H94519	GCCTGGTGT. CGAAGGT.GG TGGGCAGATG CCGGG.CCTC CATGCCTA.G	
N39798	GCCTGGTGT. CGAAGGT.GG TGGGCAGATG CCGGG.CCTC CATGCCTA.G	
H87300	.....	
R74593	.....	
R31730	.....	
R34701	.....	
H02982	.....	
R32676	.....	
T47439	.....	
R73968	.....	
H39840	.....	
H95233	.....	
H39841	.....	
N30199	.....	
T52966	.....	
N29508	.....	
N26919	.....	
N26910	.....	
H16757	.....	
N27732	.....	



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Figure 4C (Con't)

	501		550
Bikunin	G TGGT GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT ATG		
N57374	GTGGTGGT ANAATGTNAA TTAANGATTG TTGCAACTGT TTGTGTNATT		
R35464	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H94519	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
N39798	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H87300	.....		
R74593	.....		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		
	551		600
Bikunin	GGGGCTGTGA CGGAAACA GCAATAATTA CCTGACCAAG GA GGAGTGC		
N57374	GGGGCTNTTA AACGGAAANA .CAATAATNA CCTGACCAAA GAAGNAAT..		
R35464	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H94519	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
N39798	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H87300	GATTCGGCAC AGGGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTNC		
R74593	..... GCAATAATTA CCTGACCAAG GA.GGAGTGC		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

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Figure 4C (Con't)

	601				650
Bikunin	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
R35464	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
H94519	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
N39798	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
H87300	CTCAAGAAAT	GTNCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
R74593	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
R31730	.....	.....	.....	.....	.....
R34701	.....	.....	.....	.....	.....
H02982	.....	.....	.....	.....	.....
R32676	.....	.....	.....	.....	.....
T47439	.....	.....	.....	.....	.....
R73968	.....	.....	.....	.....	.....
H39840	.....	.....	.....	.....	.....
H95233	.....	.....	.....	.....	.....
H39841	.....	.....	.....	.....	.....
N30199	.....	.....	.....	.....	.....
T52966	.....	.....	.....	.....	.....
N29508	.....	.....	.....	.....	.....
N26919	.....	.....	.....	.....	.....
N26910	.....	.....	.....	.....	.....
H16757	.....	.....	.....	.....	.....
N27732	.....	.....	.....	.....	.....
	651				700
Bikunin	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
R35464	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
H94519	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
N39798	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
H87300	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
R74593	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
R31730	.....	.....	.....	.....	.....
R34701	.....	.....	.....	.....	.....
H02982	.....	.....	.....	.....	.....
R32676	.....	.....	.....	.....	.....
T47439	.....	.....	.....	.....	.....
R73968	.....	.....	.....	.....	.....
H39840	.....	.....	.....	.....	.....
H95233	.....	.....	.....	.....	.....
H39841	.....	.....	.....	.....	.....
N30199	.....	.....	.....	.....	.....
T52966	.....	.....	.....	.....	.....
N29508	.....	.....	.....	.....	.....
N26919	.....	.....	.....	.....	.....
N26910	.....	.....	.....	.....	.....
H16757	.....	.....	.....	.....	.....
N27732	.....	.....	.....	.....	.....

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Figure 4C (Con't)

	701		750
Bikunin	ATTCT GAAG ACCACTCCAG CGATATGTT CAACTAT G AAGAATACTG		
R35464	ATTCTTGAAG ACCACTTCAG CGATATGTTT CAANTATTGN AAGAATAATT		
H94519	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG		
N39798	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG		
H87300	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG		
R74593	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

	751		800
Bikunin	CACCGCCAA CGCAGT CAC TGGGCC TTG CCGTG CAT CCTT CCCAC		
R35464	GCACCGNCAA CGNATT		
H94519	GCACCGCCAA CGCATT.CAC TGGGCC..TG C.GTG.CAT. CCTT.CCCAC		
N39798	.CACCGCCAA CGCAGT.CAC TGGGGCCTTG C.GTGGAAT. CCTTTCCAC		
H87300	.CACCGCCAA CGCAGTNCAC TGGGCC.TTG C.GTGGCATN CCTT.CCCAC		
R74593	.CACCGCCAA CGCAGT.CAC TGGGCC.TTG CCGTG.CAT. CCTT.CCCAC		
R31730	.....		
R34701	.....		
H02982	.....		
R32676	.....		
T47439	.....		
R73968	.....		
H39840	.....		
H95233	.....		
H39841	.....		
N30199	.....		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

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## Figure 4C (Con't)

	801		850
Bikunin	GCTGGTACTT	T GACGTGGA GA GGAAGTC CTG CAATAA	CTTCATCTAT
H94519	GCTGGTACTT	T.GNCGT	
N39798	GCTGGNAATT	TNGACGTTGA GAAGGAAC	
H87300	GCTNGTACTT	T.GACGTGGA GA.GGAAGTC CTGGCAATAA	CTTCATCTAT
R74593	GCTGGTACTT	T.GACGTGGA GA.GGAAGTC CTG.CAATAA	CTTCATCTAT
R31730	.....	.....	.....
R34701	.....	.....	.....
H02982	.....	GA GA.GGAAGTC CTG.CAATAA	CTTCATCTAT
R32676	.....	.....	G ATTC..GGAA
T47439	.....	.....	.....
R73968	.....	.....	.....
H39840	.....	.....	.....
H95233	.....	.....	.....
H39841	.....	.....	.....
N30199	.....	.....	.....
T52966	.....	.....	.....
N29508	.....	.....	.....
N26919	.....	.....	.....
N26910	.....	.....	.....
H16757	.....	.....	.....
N27732	.....	.....	.....

	851		900
Bikunin	GGAGGCT GC	CGGGGCAAT AAGAACAG C TACCGCTC T	GAGGAGGCCT
H87300	GGAGGCTTGC	CGGGGCAATN AAGAACAGNT TACCGCTCTT	TAGGAGGCCT
R74593	GGAGGCT.GC	CGGGGCAAT. AAGAACAG.C TACCGCTC.T	GAGGAGGCCT
R31730	.....	.....G.C TACCGCTC.T	GAGGAGGCCT
R34701	.....	.....	.....
H02982	GGNGGCT.GC	CGGGG.AAT. AAGAACA.NC TACCGCTC.T	GAGGAGGCCT
R32676	CGAGGA..GC	CGGGGCAAT. AAGAACAG.C TACCGCTC.T	GAGGAGGCCT
T47439	.....	.....	....NGGCCT
R73968	.....	.....	.....
H39840	.....	.....	.....
H95233	.....	.....	.....
H39841	.....	.....	.....
N30199	.....	.....	.....
T52966	.....	.....	.....
N29508	.....	.....	.....
N26919	.....	.....	.....
N26910	.....	.....	.....
H16757	.....	.....	.....
N27732	.....	.....	.....

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Figure 4C (Con't)

	901		950
Bikunin	GCA TGCTC CGCTGCTTCC GC		CA GCAGGA
H87300	.GCA.T....		
R74593	.GCA.TGCTC CGCTGCTTCC GC.....		.CA.GCAGGA
R31730	.GCA.TGCTC CGCTGCTTCC GC.....		.CA.GCAGGA
R34701	.....TTCC GC.....		.CAAGCAGGA
H02982	.GCG.TGCTC CGCTGCTTCC GCTGTGTGT CTCTTCCAGG		CCA.GCAGGA
R32676	.GCA.TGCTC CGCTGCTTCC GC.....		.CA.GCAGGA
T47439	TGCAGTGCTC CGCTGCTTCC GC.....		.CA.GCAGGA
R73968	.....		.....
H39840	.....		.....
H95233	.....		.....
H39841	.....		.....
N30199	.....		.....
T52966	.....		.....
N29508	.....		.....
N26919	.....		.....
N26910	.....		.....
H16757	.....		.....
N27732	.....		.....
	951		1000
Bikunin	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC		TGG CGGGGC
R74593	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC		TGGCGGGGC
R31730	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC		TGG.CGGGGC
R34701	AAANTCCTCC CCTCCCCCTT GGCTCAAAGG TGGTGGTTC		TGG.CGGGGC
H02982	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC		TGG.CGGGGC
R32676	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC		TGG.CGGGGC
T47439	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC		TGG.CGGGGC
R73968	.....		....CGGGGC
H39840	.....		.....
H95233	.....		.....
H39841	.....		.....
N30199	.....		.....
T52966	.....		.....
N29508	.....		.....
N26919	.....		.....
N26910	.....		.....
H16757	.....		.....
N27732	.....		.....

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Figure 4C (Con't)

	1001				1050
Bikunin	TGTT	CGTGA	TGGTGTGAT	CC T CTTC	TGGG AGCCT CC ATGGTC
R74593	TGTT	CGTGA	TGGTGTGAT	CCTT..TTCC	TGGGGAGCCT CC.ATGGTCT
R31730	TGTT	CGTGA	TGGTGTGAT	CC.T.CTTC	TGGGGAGCCT CC.ATGGTC.
R34701	TGTT	CGTGA	TGGTGTGAT	CCCTCCTTC	CGGG.AGCCT CCCATGGTCC
H02982	TGTT	CGTGA	TGGTGTGAT	CC.T.CTTC	TGGG.AGCCT CC.ATGGTN.
R32676	TGTT	CGTGA	TGGTGTGAT	CC.T.CTTC	TGGG.AGCCT CC.ATGGTC.
T47439	TGTT	CGTGA	TGGTGTGAT	CC.T.CTTC	TGGG.AGCCT CC.ATGGTC.
R73968	TGTT	CGTGA	TGGTGTGAT	CC.T.CTTC	TGGG.AGCCT CC.ATGGTC.
H39840	.....	.....	.....	.....	.....
H95233	.....	.....	.....	.....	.....
H39841	.....	.....	.....	.....	.....
N30199	.....	.....	.....	.....	.....
T52966	.....	.....	.....	.....	.....
N29508	.....	.....	.....	.....	.....
N26919	.....	.....	.....	.....	.....
N26910	.....	.....	.....	.....	.....
H16757	.....	.....	.....	.....	.....
N27732	.....	.....	.....	.....	.....
	1051				1100
Bikunin	TACC	TGAT	CCGGGTGGCA	CGGAGG AAC C	AGG AGCG TGCCCTGCGC
R74593	TAC..	TGATT	CCGGGTGGCA	AGGAGG.AAC C.	AGG.AGCG TGCCCTGCGG
R31730	TACC	TGAT.	CCGGGTGGCA	CGGAGGGAAC C.	AGGGAGCG TGCCCTGCGC
R34701	TACCC	TGAT.	CCGGGTGGCA	CGGAGG.AAC CCAGG.	ANCG TGCCCTGCGC
H02982	TACC	TGAT.	CCGGGTNGCA	CGGAGG.AAC C.	AGGGAGCG TGCCCTGCGN
R32676	TACC	TGAT.	CCGGGTGGCA	CGGAGG.AAC C.	AGGGAGCG TGCCCTGCGC
T47439	TACC	TGAT.	CCGGGTNGCA	CGGAGG.AAC C.	AGG.AGCG TGCCCTGCGC
R73968	TACC	TGAT.	CCGGGTGGCA	CGGAGG.AAC C.	AGG.AGCG TGCCCTGCGC
H39840	.....	.....	...GGG.AAC	C.AGG.AGCG	TGCCCTGCGC
H95233	.....	.....	.....	.....	.....
H39841	.....	.....	.....	.....	.....
N30199	.....	.....	..GAGGAACC	C.ANG.AGCT	TGCCCTGCGC
T52966	.....	.....	.....	.....	.....
N29508	.....	.....	.....	.....	.....
N26919	.....	.....	.....	.....	.....
N26910	.....	.....	.....	.....	.....
H16757	.....	.....	.....	.....	.....
N27732	.....	.....	.....	.....	.....

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## Figure 4C (Con't)

	1101		1150
Bikunin	ACCG TCT G GAGCTCCGGA GATGACAAGG AGCAGCTGG TGAAGAAC		
R74593	ANCG.TCT.G GAGCTTCGGA GATGACAAGG GNT		
R31730	ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG GTGAAGAAC.		
R34701	ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.		
H02982	ACCG.TCTNG GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.		
R32676	ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG .TGAAGAAC.		
T47439	ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.		
R73968	ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.		
H39840	ACCGGTCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC.		
H95233	.....		
H39841	.....		
N30199	ACCG.TCT.G GAGCTCCGGA GATNACAANG .AGCAGCTGN .TGAAGAACC		
T52966	.....		
N29508	.....		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		
	1151		1200
Bikunin	ACATATGT C CTGT GACCG CCCTGT CGC C AAGAGG A CT GGGGAA		
R31730	ACATATGTTT CTGTTGACCG NCCTGTTCCG C.AAGAGG.A TTGGGGGAA.		
R34701	ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA.		
H02982	ACATATGT.C CTGT.GACCG NCCTGTTCCG C.AAGAGG.A CTNGGGGAAA		
R32676	ACATATGTTT CTGTTGACCG CCCTGTTCCG C.AAGAGGGA NTGGGGGAA.		
T47439	ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA.		
R73968	ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA.		
H39840	ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.NCGGAA.		
H95233	.....		
H39841	.....C. CCCTGT.CGC CAAAAGG.A CT.GGGGAA.		
N30199	ACATATGT.C CTGT.GACCG CCCTNT.CGC C.AAGAGG.A CT.GGGNAAA		
T52966	.....		
N29508	.....CC. CCCTNT.CGC C.AAGAGG.A CT.GGG.AA.		
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		

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Figure 4C (Con't)

	1201		1250
Bikunin	GGGAGGGG	AGACTAT G	TGT GA GCT TTTTTT AA A TAGA GG
R31730	.GGGAGGGG	A	
R34701	.GGGAGGGG	AGACTAT.G.	TGT.GA.GCT TTTTTT..AA A.TA
H02982	GGGAGGGG	AGATTAT.G.	TGTGA.GTT TTTTTT..AA ANTAG
R32676	GGGAGGGG	AGANTATGT	TGTGA.GNT TTTTTTAA ATTAGGAGGG
T47439	.GGGAGGGG	AGACTAT.G.	TGT.GA.GCT TTTTTT..AA A.TAGA..GG
R73968	.GGGAGGGG	AGACTAT.G.	TGT.GA.GCT TTTTTT..AA A.TAGA..GG
H39840	.GGGAGGGG	AGACTAT.G.	TGT.GA.GCT TTTTTT..AA A.TAGA..GG
H95233	.....		
H39841	.GGGAGGGG	AAACNAT.G.	TGT.GAACCT TTTTTT.AAA A.TAGA..GG
H30199	.GGGAGGGG	AGACTAT.G.	TGT.AA.GCT TTTTTT..AA A.TAGA..GG
T52966	.....		
N29508	.GGGAGGGG	AGACTA..G.	TGT.GA.GCT TTTTTT..AA A.TAGA..GG
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		
	1251		1300
Bikunin	GATTGACTC	GGATTTC A	GT GATC A TTAGGG CT GAGGTCTGTT
R32676	GNTTGANTTC	GGGNTTTTNA	GTTGATCCAT TTAGGGGGNT GAG
T47439	GATTGACTC.	.GGATTTC.A	GT.GATC.A. TTAGGG..CT GAGGTCTGTT
R73968	GATTGACTC.	.GGATTTC.A	GT.GATC.A. TTAGGG..CT GAGGTCTGTT
H39840	GATTGACTC.	.GGATTTC.A	GT.GATC.A. TTAGGG..CT GAGGTCTGTT
H95233	.....	.....A.	TTAGGG..CT GAGGTCTGTT
H39841	GATTGACTC.	.GGATTTC.A	GT.GATC.A. TTAGGG..CT GAGGTCTGTT
N30199	GATTGACTC.	.GGATTTCGA	GT.GATC.A. TTAGGG..CT GAGGTCTGTT
T52966	.....		
N29508	GATTGACTC.	.GGATTTC.A	GT.GATCNA. TTAGGG..CT GAGGTCTGTT
N26919	.....		
N26910	.....		
H16757	.....		
N27732	.....		
	1301		1350
Bikunin	TCTCTGGGAG	GTAGGACGGC	TGCTTCG TG G TC TGGCA GGGATGGG
T47439	TCTCTGGGAG	GTAGGACGA	
R73968	TCTCTGGGAG	GTAGGACGGC	TGCTTCG TG GGTCTGGCA .GGGATGGG
H39840	TCTCTGGGAG	GTAGGACGGC	TGCTTCG TG G.TC.TGGCA .GGGATGGG.
H95233	NCCTCTGGGAG	NTAGGACGGC	TGCTTCCTG G.TC.TGGCA .GGGATGGG.
H39841	TCNCTGGGAG	GTAGGACGGC	TGCTTCCTG G.TC.TGGCA .GGGATGGG.
N30199	TCTCTGGGAG	GTAGGACGGC	TGCTTCG TG G.TC.TGGCA .GGGATGGG.
T52966	.....	.....	.....TC.TGGCA .GGGATGGG.
N29508	TCTCTGGGAG	GTAGGACGGC	TGCTTCG TG G.TC.TGGCA .GGGATGGG.
N26919	.....		
N26910	.....		
H16757	.....	.....G	G.TC.TGGCA .GGGATGGG.
N27732	.....	.....CGCTG	GGTCTGCA AGGNATGGG



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Figure 4C (Con't)

1351 1400  
 Bikunin TTTG CTTTG G AAATCCTC T AGGAGGCT CCTCCT CGC ATGG CC TG  
 R73968 TTTG.CTTTG GGAAATCCTC TTNGGAGGCT CCTCCTTCGC ATGGGCTTG  
 H39840 TTTG.CTTTG GAGAATCCTC T.ANGAGGCT CCTCCT.CGC ATGG.CC.TG  
 H95233 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 H39841 TTTG.CTTTG G.AAANCNC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N30199 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCTTCGC ATGG.CC.TG  
 T52966 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N29508 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N26919 ..... GAGGCT CCTCCT.CGC ATGG.CC.TG  
 N26910 .....CTTTT GNAAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 H16757 TTTGCCTTTG G.AAANCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG  
 N27732 TTTG.CTTTG G.AAATCCTC TTAGGAGGCT CCTCCT.CGC ATGG.CC.TG

1401 1450  
 Bikunin CAGT CT GG CAGCAG CCC CGAGTTGTTT CC TCGCTG ATC GATTTC  
 R73968 CAGT.CTNGG CAGCANCCCC CGAGTTTTTT TCCTTCGCTG ATCCGATTTC  
 H39840 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 H95233 CAGTTCT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 H39841 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTN .CC.TCGCTG ATC.GATNTC  
 N30199 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 T52966 CAGT.CT.GG CAGCAG..CC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 N29508 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 N26919 CAGT.CTTGG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC  
 N26910 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATCGGATTTC  
 H16757 CAGTNCCT.GG CAGCAGACCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC  
 N27732 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC

1451 1500  
 Bikunin TTT CCTCCA GGTAG AGT TTTC TTG CTTATGTTGA ATTCCATTGC  
 R73968 TTTTCCTCCA GGTAGAATT TTTCTTTT  
 H39840 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 H95233 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 H39841 TTT.CCCCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 N30199 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 T52966 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 N29508 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 N26919 TTT.CCNCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 N26910 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC  
 H16757 TTTACCCCA GGTAG..AGT TTTCCTTGN CTTATGTTGA ATTCCATTGC  
 N27732 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC

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Figure 4C (Con't)

1501 1550  
Bikunin CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT  
H39840 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTTGT  
H95233 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
H39841 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
N30199 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
T52966 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
N29508 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
N26919 CTCTTTT.CN CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
N26910 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
H16757 CTCTTTTACT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT  
N27732 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT

1551 1600  
Bikunin CTGATTTATG G TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
H39840 CTGATTTATG GGTTTTTTT AAGTAT  
H95233 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
H39841 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
N30199 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
T52966 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
N29508 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
N26919 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
N26910 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
H16757 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT  
N27732 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT

1601 1650  
Bikunin CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
H95233 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAA  
H39841 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
N30199 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
T52966 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
N29508 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
N26919 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
N26910 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
H16757 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC  
N27732 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC

1651 1689  
Bikunin CTTTAG AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  
H39841 CTTTAA.  
N30199 CTTTAG.AAT AAA  
T52966 CTTTAGGAAT NAAAAA AAAAGGTC  
N29508 CTTTAG.AAT AAATTCAGC ATGTGCTTTC AA  
N26919 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA A  
N26910 CTTTAG.AAT AAATTCAGC ATGTGCTTTC AAAAAA  
H16757 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAA  
N27732 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

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## FIGURE 4D

EST consensus MLRAEADGVS RLLGSLLLLSG VLAADRERSI HDFCLVSKVV GCRASMPRW 50  
EST consensus WYNVTDGSCQ LFVYGGCDGN SNNYLTKEEC LKKCATVTEN ATGDLATSRN 100  
EST consensus AADSSVPSAP RRQDSEDHSS DMFNYYEYCT ANAVTGPCRA SFPRWYFDVE 150  
EST consensus RNSCNNFIYG GCRGNKNSYR SEEACMLRCF RQENPPLPL GSKYVVL~~AGL~~ 200  
EST consensus FVMVLILELG ASMYLIRVA RRNQERALRT VWSSGDDKEQ LVKNTYVL 248

cDNA								ACC	3
translation								T	-47
cDNA	TGATCGCGAG	ACCCCCAACGG	CTGGTGGCGT	CGCCTGCGCG	TCTCGGCTGA				53
translation	. S R D	P N G	W W R	R L R V	S A E				-30
cDNA	GCTGGCCATG	GCGCAGCTGT	GCGGGCTGAG	GCGGAGCCGG	GCGTTTCTCG				103
translation	L A M	A Q L C	G L R	R S R	A F L A				-13
cDNA	CCCTGCTGGG	ATCGCTGCTC	CTCTCTGGGG	TCCTGGCGGC	CGACCGAGAA				153
translation	L L G	S L L	L S G V	L A A	D R E				4
cDNA	CGCAGCATCC	ACGACTTCTG	CCTGGTGTCTG	AAGGTGGTGG	GCAGATGCCG				203
translation	R S I H	D F C	L V S	K V V G	R C R				21
cDNA	GGCCTCCATG	CCTAGGTGGT	GGTACAATGT	CACTGACGGA	TCCTGCCAGC				253
translation	A S M	P R W W	Y N V	T D G	S C Q L				38
cDNA	TGTTTGTGTA	TGGGGGCTGT	GACGGAACA	GCAATAATTA	CCTGACCAAG				303
translation	F V Y	G G C	D G N S	N N Y	L T K				54
cDNA	GAGGAGTGCC	TCAAGAAATG	TGCCACTGTC	ACAGAGAATG	CCACGGGTGA				353
translation	E E C L	K K C	A T V	T E N A	T G D				71
cDNA	CCTGGCCACC	AGCAGGAATG	CAGCGGATTC	CTCTGTCCCA	AGTGCTCCCA				403
translation	L A T	S R N A	A D S	S V P	S A P R				88
cDNA	GAAGGCAGGA	TTCTGAAGAC	CACTCCAGCG	ATATGTTCAA	CTATGAAGAA				453
translation	R Q D	S E D	H S S D	M F N	Y E E				104
cDNA	TACTGCACCG	CCAACGCAGT	CACTGGGCCT	TGCCGTGCAT	CCTTCCCACG				503
translation	Y C T A	N A V	T G P	C R A S	F P R				121
cDNA	CTGGTACTTT	GACGTGGAGA	GGAACCTCTG	CAATAACTTC	ATCTATGGAG				553
translation	W Y F	D V E R	N S C	N N F	I Y G G				138
cDNA	GCTGCCGGGG	CAATAAGAAC	AGCTACCGCT	CTGAGGAGGC	CTGCATGCTC				603
translation	C R G	N K N	S Y R S	E E A	C M L				154
cDNA	CGCTGCTTCC	GCCAGCAGGA	GAATCCTCCC	CTGCCCCCTTG	GCTCAAAGGT				653
translation	R C F R	Q Q E	N P P	L P L G	S K Y				171
cDNA	GGTGGTTCTG	GCGGGGCTGT	TCGTGATGGT	GTTGATCCTC	TTCTGGGAG				703
translation	<u>V V L A G L F</u>	<u>V M V L I L F</u>	<u>L L G A</u>						188
cDNA	CCTCCATGGT	CTACCTGATC	CGGGTGGCAC	GGAGGAACCA	GGAGCGTGCC				753
translation	<u>S M V Y L I</u>	<u>R V A R</u>	<u>R N Q</u>	<u>E R A</u>					204
cDNA	CTGCGCACCG	TCTGGAGCTT	CGGAGATGA						792
translation	L R T V	W S F	G D						213

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## FIGURE 4F

cDNA GCACGAGTTG GGAGGTGTAG CGCGGCTCTG AACGCGCTGA GGGCCGTTGA 50  
 cDNA GTGTGCGCAGG CGGCGAGGGC GCGAGTGAGG AGCAGACCCA GGCATCGCGC 100  
 cDNA GCCGAGAAGG CCGGGCGTCC CCACACTGAA GGTCCGGAAA GGCGACTTCC 150  
 cDNA GGGGGCTTTG GCACCTGGCG GACCCCTCCG GAGCGTCGGC ACCTGAACGC 200  
 cDNA GAGGCGCTCC ATTGCGCGTG CGCGTTGAGG GGCTTCCCGC ACCTGATCGC 250  
 cDNA GAGACCCCAA CGGCTGGTGG CGTCGCCTGC GCGTCTCGGC TGAGCTGGCC 300  
 cDNA ATGGCGCAGC TGTGCGGGCT GAGGCGGAGC CGGGCGTTTC TCGCCCTGCT 350  
 translation M A Q L C G L R R S R A F L A L L -11

cDNA GGGATCGCTG CTCCTCTCTG GGGTCCTGGC GGCCGACCGA GAACGCAGCA 400  
 translation G S L L L S G V L A A D R E R S I 7

cDNA TCCACGACTT CTGCCTGGTG TCGAAGGTGG TGGGCAGATG CCGGGCCTCC 450  
 translation H D F C L V S K V V G R C R A S 23

cDNA ATGCCTAGGT GGTGGTACAA TGTCACTGAC GGATCCTGCC AGCTGTTTGT 500  
 translation M P R W W Y N V T D G S C Q L F V 40

cDNA GTATGGGGGC TGTGACGGAA ACAGCAATAA TTACCTGACC AAGGAGGAGT 550  
 translation Y G G C D G N S N N Y L T K E E C 57

cDNA GCCTCAAGAA ATGTGCCACT GTCACAGAGA ATGCCACGGG TGACCTGGCC 600  
 translation L K K C A T V T E N A T G D L A 73

cDNA ACCAGCAGGA ATGCAGCGGA TTCCTCTGTC CCAAGTGCTC CCAGAAGGCA 650  
 translation T S R N A A D S S V P S A P R R Q 90

cDNA GGATTCTGAA GACCACTCCA GCGATATGTT CAACTATGAA GAATACTGCA 700  
 translation D S E D H S S D M F N Y E E Y C T 107

cDNA CCGCCAACGC AGTCACTGGG CTTGCGGTG CATCCTTCCC ACGCTGGTAC 750  
 translation A N A V T G P C R A S F P R W Y 123

cDNA TTTGACGTGG AGAGGAATC CTGCAATAAC TTCATCTATG GAGGCTGCCG 800  
 translation F D V E R N S C N N F I Y G G C R 140

cDNA GGGCAATAAG AACAGCTACC GCTCTGAGGA GGCCTGCATG CTCCGCTGCT 850  
 translation G N K N S Y R S E E A C M L R C F 157

cDNA TCCGCCAGCA GGAGAATCCT CCCCTGCCCC TTGGCTCAAA GGTGGTGGTT 900  
 translation R Q Q E N P P L P L G S K V V V 173

cDNA CTGGCGGGGC TGTTCGTGAT GGTGTTGATC CTCTTCCTGG GAGCCTCCAT 950  
 translation L A G L F V M V L L L F L G A S M 190

cDNA GGTCTACCTG ATCCGGGTGG CACGGAGGAA CCAGGAGCGT GCCCTGCGCA 1000  
 translation V Y L I R V A R R N Q E R A L R T 207

cDNA CCGTCTGGAG CTCCGAGAT GACAAGGAGC AGCTGGTGAA GAACACATAT 1050  
 translation V W S S G D D K E Q L V K N T Y 223

cDNA GTCCTGTGAC CGCCCTGTGG CCAAGAGGAC TGGGGAAGGG AGGGGAGACT 1100  
 translation V L \* 225

## FIGURE 4F (Con't)

cDNA	ATGTGTGAGC	TTTTTTTAAA	TAGAGGGATT	GACTCGGATT	TGAGTGATCA	1150
cDNA	TTAGGGCTGA	GGTCTGTTTC	TCTGGGAGGT	AGGACGGCTG	CTTCCTGGTC	1200
cDNA	TGGCAGGGAT	GGGTTTGCTT	TGGAAATCCT	CTAGGAGGCT	CCTCCTCGCA	1250
cDNA	TGGCCTGCAG	TCTGGCAGCA	GCCCCGAGTT	GTTTCCTCGC	TGATCGATTT	1300
cDNA	CTTTCCTCCA	GGTAGAGTTT	TCTTTGCTTA	TGTTGAATTC	CATTGCCTCC	1350
cDNA	TTTTCTCNAT	CACAGAAGTG	ATGTTGGAAT	CGTTTCTTTT	GTTTGTCTGA	1400
cDNA	TTTATGGTTT	TTTTAAGTAT	AAACAAAAGT	TTTTTATTAG	CATTCTGAAA	1450
cDNA	GAAGGAAAGT	AAAAATGTACA	AGTTTAATAA	AAAGGGGCCT	TCCCCTTTAG	1500
cDNA	AATAAATTC	CAGCATGTTG	CTTTCAAAAA	AAAAAAAAAA	AAAA	

1550

## FIGURE 4G

EST consensus	MLR AEADGVSRLI GSLLLSGVLA	-1
PCR clone	MAQLCGL RRSRAFLALL GSLLLSGVLA	-1
λcDNA clone	MAQLCGL RRSRAFLALL GSLLLSGVLA	-1
EST consensus	ADRERSIHDF CLVSKVVGRC RASMPRWYN VTDGSCQLFV YGGCDGNSNN	50
PCR clone	ADRERSIHDF CLVSKVVGRC RASMPRWYN VTDGSCQLFV YGGCDGNSNN	50
λcDNA clone	ADRERSIHDF CLVSKVVGRC RASMPRWYN VTDGSCQLFV YGGCDGNSNN	50
EST consensus	YLTKEECLKK CATVTENATG DLATSRNAAD SSVPSAPRRQ DSEDHSSDMF	100
PCR clone	YLTKEECLKK CATVTENATG DLATSRNAAD SSVPSAPRRQ DSEDHSSDMF	100
λcDNA clone	YLTKEECLKK CATVTENATG DLATSRNAAD SSVPSAPRRQ DSEDHSSDMF	100
EST consensus	NYEEYCTANA VTGPCRASFP RWYFDVERNS CNNFIYGGCR GNKNSYRSEE	150
PCR clone	NYEEYCTANA VTGPCRASFP RWYFDVERNS CNNFIYGGCR GNKNSYRSEE	150
λcDNA clone	NYEEYCTANA VTGPCRASFP RWYFDVERNS CNNFIYGGCR GNKNSYRSEE	150
EST consensus	ACMLRCFRQQ ENPPLPLGSK <u>VVVLAGEFVM VLLELFGASM VYLIRVARRN</u>	200
PCR clone	ACMLRCFRQQ ENPPLPLGSK <u>VVVLAGEFVM VLLELFGASM VYLIRVARRN</u>	200
λcDNA clone	ACMLRCFRQQ ENPPLPLGSK <u>VVVLAGEFVM VLLELFGASM VYLIRVARRN</u>	200
EST consensus	QERALRTVWS SGDDKEQLVK NTYVL	225
PCR clone	QERALRTVWS FGD	213
λcDNA clone	QERALRTVWS SGDDKEQLVK NTYVL	225

## Purification of Placental Bikunin using Superdex 75 Gel-Filtration

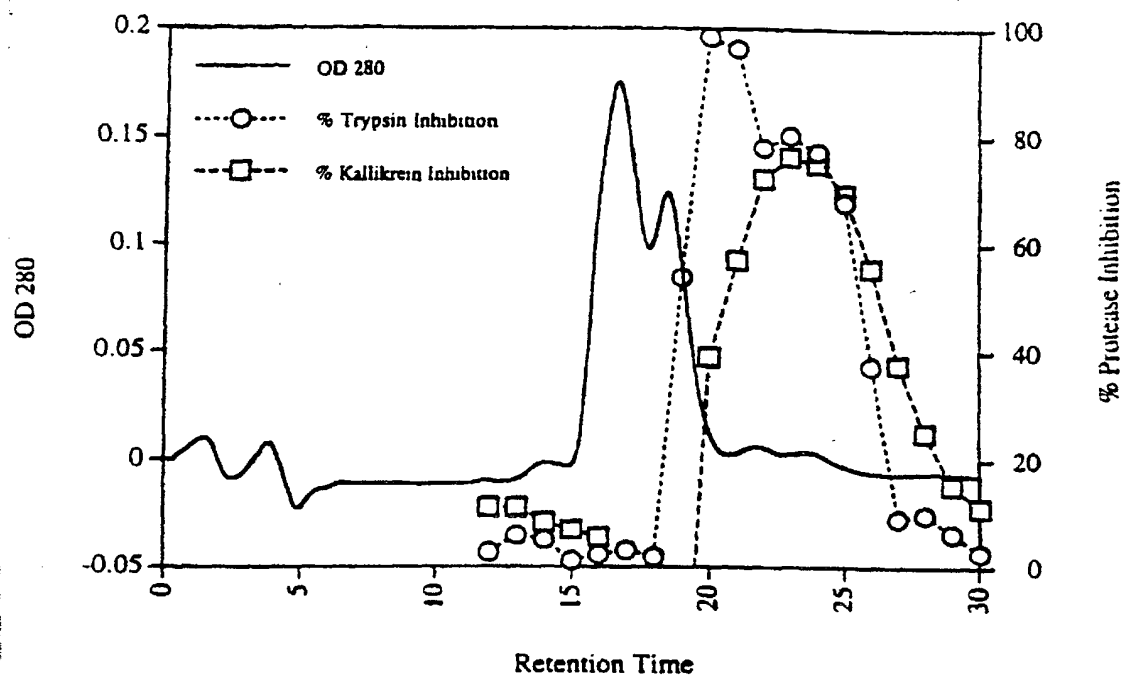
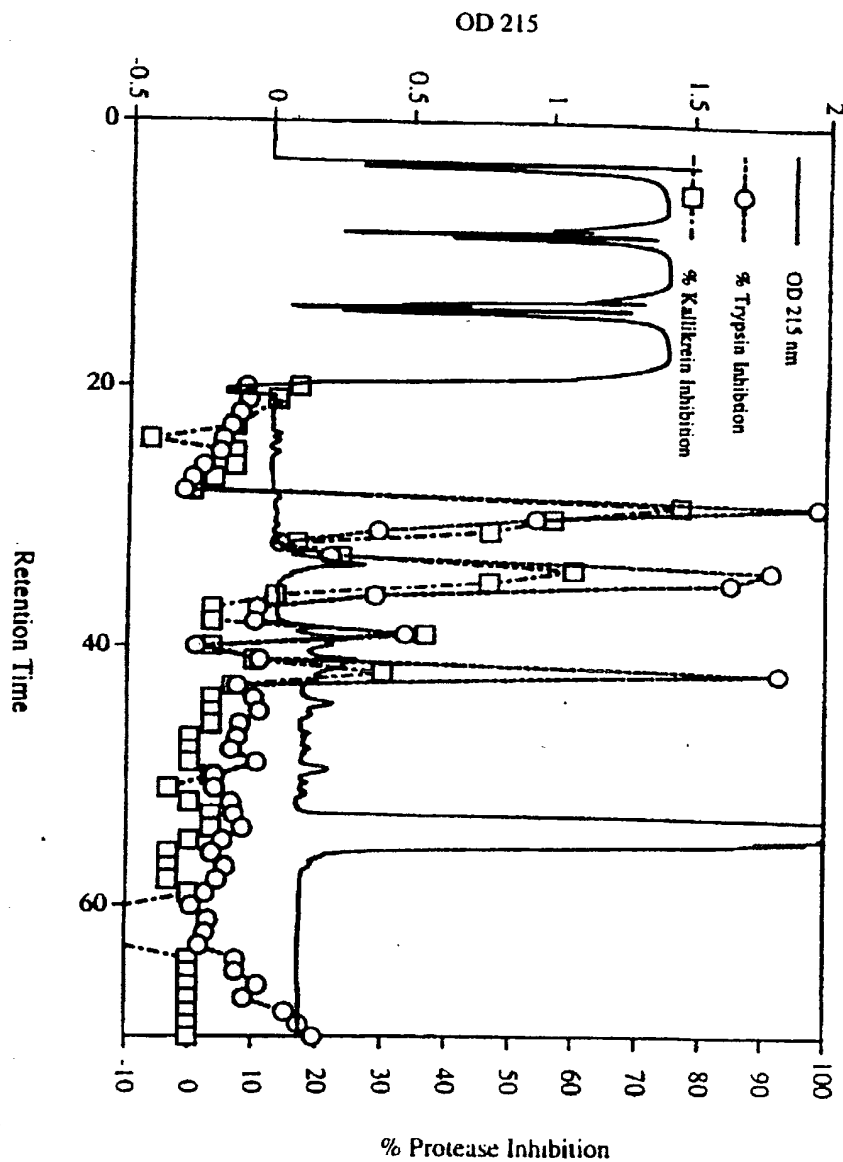


FIGURE 5



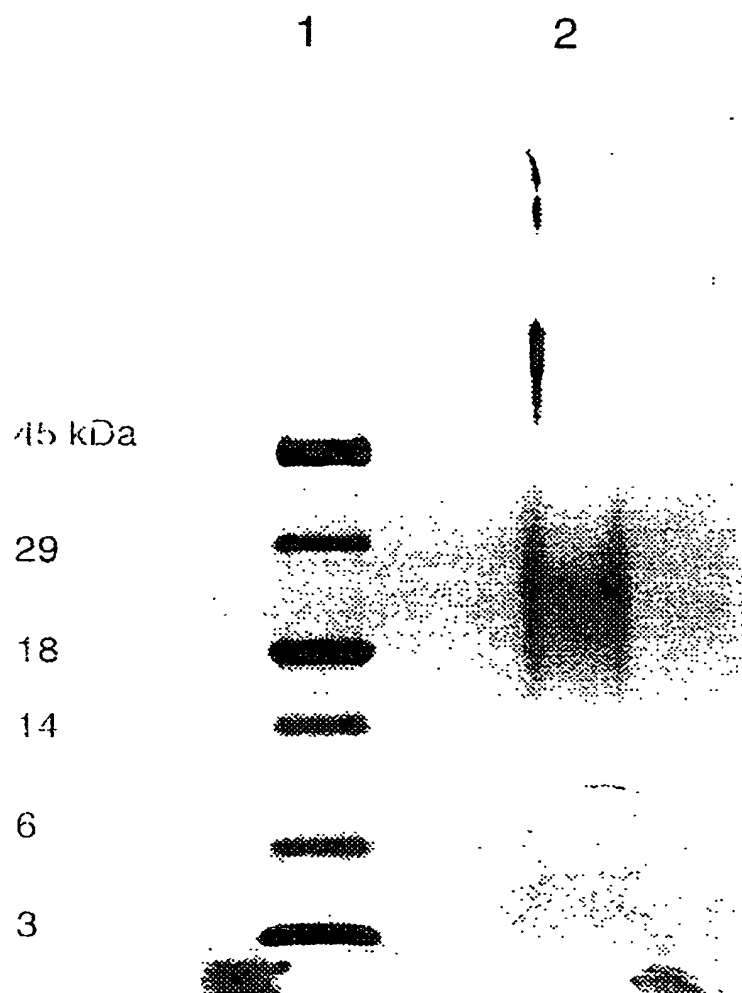
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Purification of Placental Bikunin using C18 Reverse-Phase Chromatography

FIGURE 6

**Figure 7**



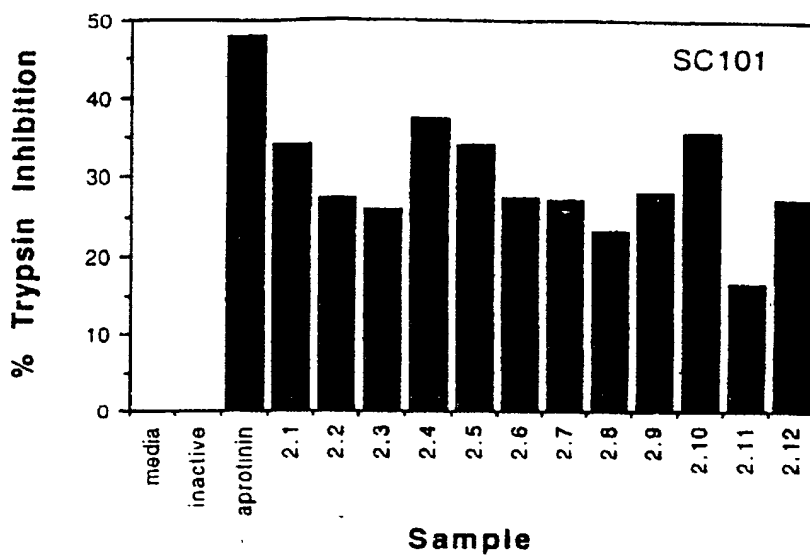
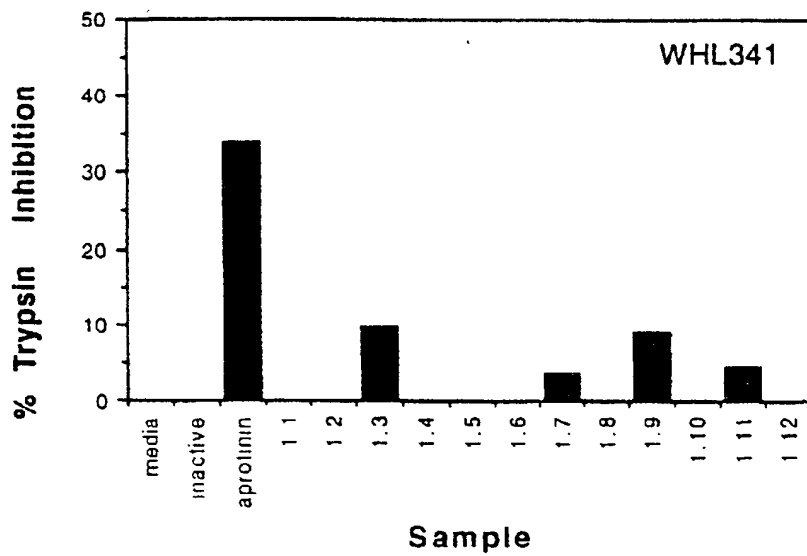
**Figure 8A****Figure 8B**

Figure 9A

SDS-PAGE

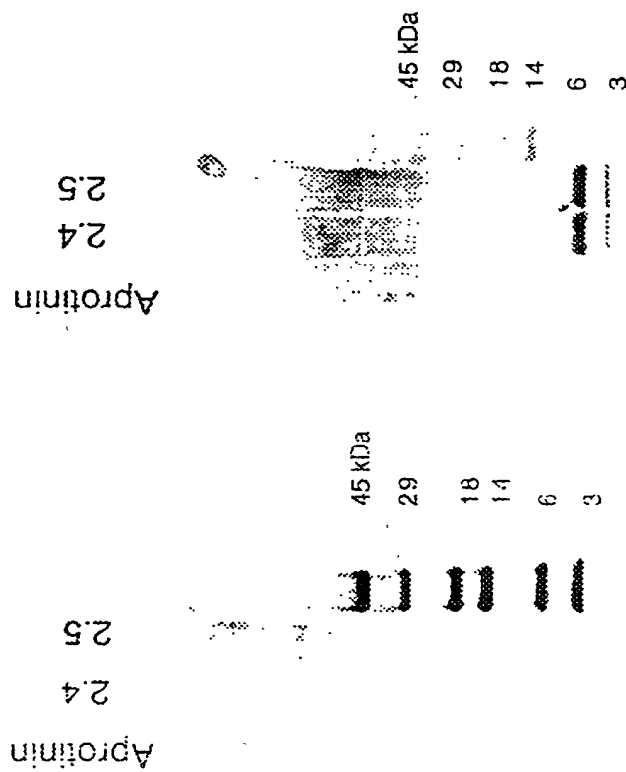
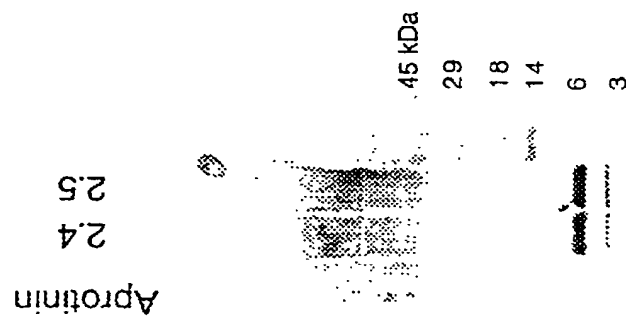


Figure 9B

Western



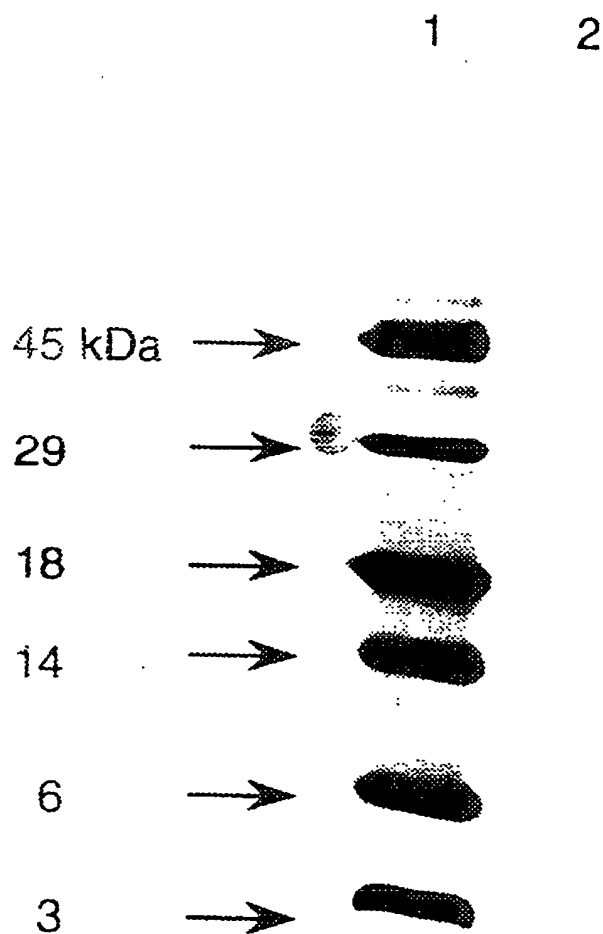
**Figure 10**

FIG. 11A

Figure 11A

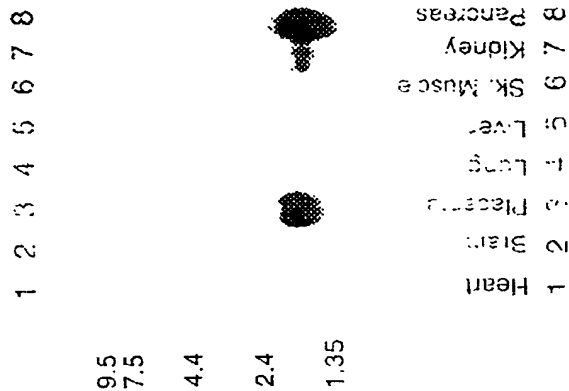


Figure 11B

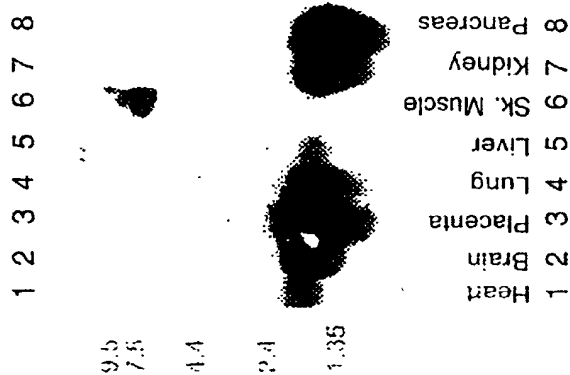


Figure 12A  
Figure 12B

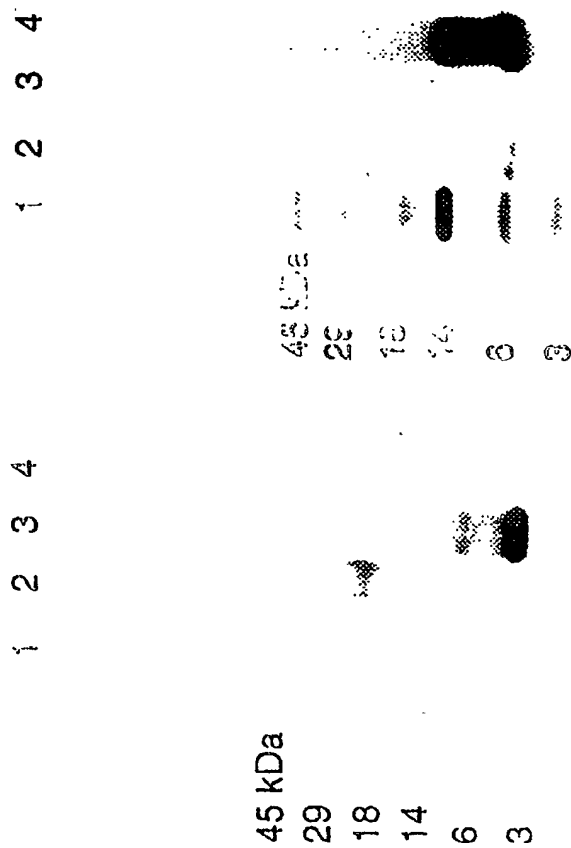


Figure 13

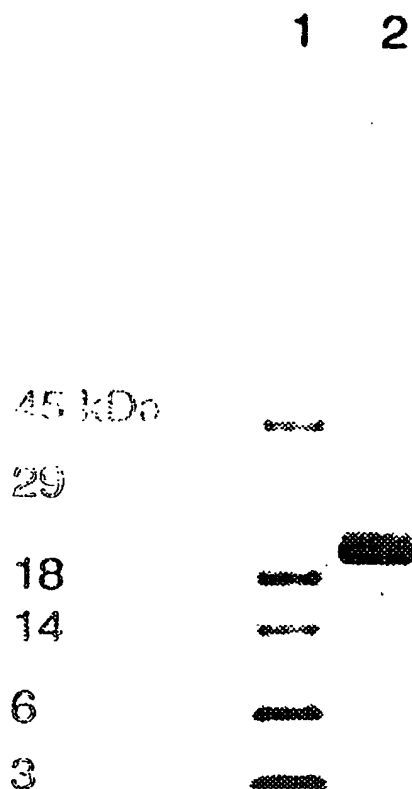




Figure 14

